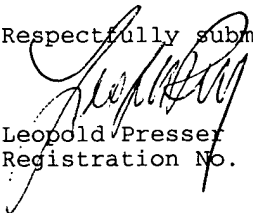


REMARKS

It is respectfully requested that this Preliminary  
Amendment be entered in this application prior to examination.  
Early and favorable consideration is requested.

Respectfully submitted,

  
Leopold Presser  
Registration No. 19,827

SCULLY, SCOTT, MURPHY & PRESSER  
400 Garden City Plaza  
Garden City, New York 11530  
(516) 742-4343

LP:ae

09037657.034098

# SEQUENCE LISTING

<110> Hilton, Douglas J.  
Nicola, Nicos A.  
Farley, Alison  
Wilson, Tracy  
Zhang, Jian-Guo  
Alexander, Warren  
Rakar, Steven  
Fabri, Louis  
Kojima, Tetsuo  
Maeda, Masatsugu  
Kikuchi, Yasufumi  
Nash, Andrew

<120> A NOVEL HAEMPOIETIN RECEPTOR AND GENETIC SEQUENCES  
ENCODING SAME

<130> DAVIES COLLISON CAVE (CIP)

<140> 09/037,657

<141> 1998-03-10

<150> 08/928,720

<151> 1997-09-11

<160> 54

<170> PatentIn Ver. 2.0

<210> 1

<211> 5

<212> PRT

<213> Unknown

<220>

<221> UNSURE

<222> (3)

<223> Unsure at position 3

<400> 1

Trp Ser Xaa Trp Ser  
1 5

<210> 2

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: M116 probe

<400> 2

actcgctcca gattcccgcc tttt

24

<210> 3  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:M108 probe

<400> 3  
tcccgcccttt ttcgacccat agat 24

<210> 4  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:M159 probe

<400> 4  
ggtacttggc ttggaagagg aaat 24

<210> 5  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:M242 probe

<400> 5  
cggctcacgt gcacgtcggg tggg 24

<210> 6  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:M112 probe

<400> 6  
agctgctggt aaagggcttc tc 22

<210> 7  
<211> 15  
<212> DNA  
<213> Unknown

<220>  
<223> Description of Unknown Organism:Unsure

<220>

<221> unsure  
<222> (1)  
<223> Unsure at position 1

<220>  
<221> unsure  
<222> (7)  
<223> Unsure at position 7

<220>  
<221> unsure  
<222> (10)  
<223> Unsure at position 10

<400> 7  
rctccartcr ctcca

15

<210> 8  
<211> 15  
<212> DNA  
<213> Unknown

<220>  
<223> Description of Unknown Organism:Unsure

<220>  
<221> unsure  
<222> (1)  
<223> Unsure at position 1

<220>  
<221> unsure  
<222> (7)  
<223> Unsure at position 7

<220>  
<221> unsure  
<222> (10)  
<223> Unsure at position 10

<400> 8  
rctccaytcr ctcca

15

<210> 9  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:1944 probe

<400> 9  
aagtgtgacc atcatgtgga c

21

<210> 10  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:2106 probe

<400> 10  
 ggaggtgtta aggaggcg 18

<210> 11  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:2120 probe

<400> 11  
 atgcccgcgg gtcgcccg 18

<210> 12  
 <211> 1629  
 <212> DNA  
 <213> Unknown

<220>  
 <221> CDS  
 <222> (124)..(1362)

<220>  
 <223> Description of Unknown Organism:Murine NR6.1

<400> 12  
 ggcacgagct tcgctgtccg cgcccagtga cgcgcgtgcg gacccgagcc ccaatctgca 60  
 ccccgagac tcgccccgc ccataccgg cgttgagtc accgcccgtt gcgcgccacc 120  
 ccc atg ccc gcg ggt cgc ccg gcc ccc gtc gcc caa tcc gcg cgg cgg 168  
 Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg  
 1 5 10 15  
 ccg ccg cgg ccg ctg tcc tcg ctg tgg tcg cct ctg ttg ctc tgt gtc 216  
 Pro Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val  
 20 25 30  
 ctc ggg gtg cct cgg ggc gga tgg gga gcc cac aca gct gta atc agc 264  
 Leu Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser  
 35 40 45  
 ccc cag gac ccc acc ctt ctc atc ggc tcc tcc ctg caa gct acc tgc 312  
 Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys  
 50 55 60

tct	ata	cat	gga	gac	aca	cct	ggg	gcc	acc	gct	gag	ggg	ctc	tac	tgg	360
Ser	Ile	His	Gly	Asp	Thr	Pro	Gly	Ala	Thr	Ala	Glu	Gly	Leu	Tyr	Trp	
	65					70					75					
acc	ctc	aat	ggt	cgc	cgc	ctg	ccc	tct	gag	ctg	tcc	cgc	ctc	ctt	aac	408
Thr	Leu	Asn	Gly	Arg	Arg	Leu	Pro	Ser	Glu	Leu	Ser	Arg	Leu	Leu	Asn	
	80				85					90					95	
acc	tcc	acc	ctg	gcc	ctg	gcc	ctg	gct	aac	ctt	aat	ggg	tcc	agg	cag	456
Thr	Ser	Thr	Leu	Ala	Leu	Ala	Leu	Ala	Asn	Leu	Asn	Gly	Ser	Arg	Gln	
				100					105					110		
cag	tca	gga	gac	aat	ctg	gtg	tgt	cac	gcc	cga	gac	ggc	agc	att	ctg	504
Gln	Ser	Gly	Asp	Asn	Leu	Val	Cys	His	Ala	Arg	Asp	Gly	Ser	Ile	Leu	
			115					120					125			
gct	ggc	tcc	tgc	ctc	tat	gtt	ggc	ttg	ccc	cct	gag	aag	ccc	ttt	aac	552
Ala	Gly	Ser	Cys	Leu	Tyr	Val	Gly	Leu	Pro	Pro	Glu	Lys	Pro	Phe	Asn	
		130					135					140				
atc	agc	tgc	tgg	tcc	cgg	aac	atg	aag	gat	ctc	acg	tgc	cgc	tgg	aca	600
Ile	Ser	Cys	Trp	Ser	Arg	Asn	Met	Lys	Asp	Leu	Thr	Cys	Arg	Trp	Thr	
	145					150					155					
ccg	ggt	gca	cac	ggg	gag	aca	ttc	tta	cat	acc	aac	tac	tcc	ctc	aag	648
Pro	Gly	Ala	His	Gly	Glu	Thr	Phe	Leu	His	Thr	Asn	Tyr	Ser	Leu	Lys	
	160				165					170					175	
tac	aag	ctg	agg	tgg	tac	ggt	cag	gat	aac	aca	tgt	gag	gag	tac	cac	696
Tyr	Lys	Leu	Arg	Trp	Tyr	Gly	Gln	Asp	Asn	Thr	Cys	Glu	Glu	Tyr	His	
			180					185						190		
act	gtg	ggc	cct	cac	tca	tgc	cat	atc	ccc	aag	gac	ctg	gcc	ctc	ttc	744
Thr	Val	Gly	Pro	His	Ser	Cys	His	Ile	Pro	Lys	Asp	Leu	Ala	Leu	Phe	
			195					200					205			
act	ccc	tat	gag	atc	tgg	gtg	gaa	gcc	acc	aat	cgc	cta	ggc	tca	gca	792
Thr	Pro	Tyr	Glu	Ile	Trp	Val	Glu	Ala	Thr	Asn	Arg	Leu	Gly	Ser	Ala	
		210					215					220				
aga	tct	gat	gtc	ctc	aca	ctg	gat	gtc	ctg	gac	gtg	gtg	acc	acg	gac	840
Arg	Ser	Asp	Val	Leu	Thr	Leu	Asp	Val	Leu	Asp	Val	Val	Thr	Thr	Asp	
	225					230					235					
ccc	cca	ccc	gac	gtg	cac	gtg	agc	cgc	gtt	ggg	ggc	ctg	gag	gac	cag	888
Pro	Pro	Pro	Asp	Val	His	Val	Ser	Arg	Val	Gly	Gly	Leu	Glu	Asp	Gln	
	240				245					250					255	
ctg	agt	gtg	cgc	tgg	gtc	tca	cca	cca	gct	ctc	aag	gat	ttc	ctc	ttc	936
Leu	Ser	Val	Arg	Trp	Val	Ser	Pro	Pro	Ala	Leu	Lys	Asp	Phe	Leu	Phe	
				260					265					270		
caa	gcc	aag	tac	cag	atc	cgc	tac	cgc	gtg	gag	gac	agc	gtg	gac	tgg	984
Gln	Ala	Lys	Tyr	Gln	Ile	Arg	Tyr	Arg	Val	Glu	Asp	Ser	Val	Asp	Trp	
			275				280						285			
aag	gtg	gtg	gat	gac	gtc	agc	aac	cag	acc	tcc	tgc	cgt	ctc	gcg	ggc	1032

Lys	Val	Val	Asp	Asp	Val	Ser	Asn	Gln	Thr	Ser	Cys	Arg	Leu	Ala	Gly		
		290					295					300					
ctg	aag	ccc	ggc	acc	gtt	tac	ttc	gtc	caa	gtg	cgt	tgt	aac	cca	ttc	1080	
Leu	Lys	Pro	Gly	Thr	Val	Tyr	Phe	Val	Gln	Val	Arg	Cys	Asn	Pro	Phe		
	305					310					315						
ggg	atc	tat	ggg	tcg	aaa	aag	gcg	gga	atc	tgg	agc	gag	tgg	agc	cac	1128	
Gly	Ile	Tyr	Gly	Ser	Lys	Lys	Ala	Gly	Ile	Trp	Ser	Glu	Trp	Ser	His		
320					325					330					335		
ccc	acc	gct	gcc	tcc	acc	cct	cga	agt	gag	cgc	ccg	ggc	ccg	ggc	ggc	1176	
Pro	Thr	Ala	Ala	Ser	Thr	Pro	Arg	Ser	Glu	Arg	Pro	Gly	Pro	Gly	Gly		
				340					345					350			
ggg	gtg	tgc	gag	ccg	cgg	ggc	ggc	gag	ccc	agc	tcg	ggc	ccg	gtg	cgg	1224	
Gly	Val	Cys	Glu	Pro	Arg	Gly	Gly	Glu	Pro	Ser	Ser	Gly	Pro	Val	Arg		
			355					360					365				
cgc	gag	ctc	aag	cag	ttc	ctc	ggc	tgg	ctc	aag	aag	cac	gca	tac	tgc	1272	
Arg	Glu	Leu	Lys	Gln	Phe	Leu	Gly	Trp	Leu	Lys	Lys	His	Ala	Tyr	Cys		
		370					375					380					
tcg	aac	ctt	agt	ttc	cgc	ctg	tac	gac	cag	tgg	cgt	gct	tgg	atg	cag	1320	
Ser	Asn	Leu	Ser	Phe	Arg	Leu	Tyr	Asp	Gln	Trp	Arg	Ala	Trp	Met	Gln		
	385					390					395						
aag	tca	cac	aag	acc	cga	aac	cag	gtc	ctg	ccg	gct	aaa	ctc			1362	
Lys	Ser	His	Lys	Thr	Arg	Asn	Gln	Val	Leu	Pro	Ala	Lys	Leu				
400					405					410							
taaggatagg ccattctctt gctgggtcag acctggaggc tcacctgaat tggagcccct																1422	
ctgtaccatc tgggcaacaa agaaacctac cagaggctgg ggcacaatga gctcccacaa																1482	
ccacagcttt ggtccacatg atggtcacac ttggatatac cccagtgtgg gtaaggttgg																1542	
ggtattgcag ggcctcccaa caatctcttt aaataaataa aggagttggt caggtaaaaa																1602	
aaaaaaaaa aaaaaaaaaa aaaaaaa																1629	

<210> 13  
 <211> 413  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Description of Unknown Organism: Murine NR6.1

<400> 13  
 Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg Pro  
 1 5 10 15  
 Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val Leu  
 20 25 30





Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Gly  
 340 345 350  
 Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg  
 355 360 365  
 Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser  
 370 375 380  
 Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys  
 385 390 395 400  
 Ser His Lys Thr Arg Asn Gln Val Leu Pro Ala Lys Leu  
 405 410

<210> 14  
 <211> 1673  
 <212> DNA  
 <213> Unknown

<220>  
 <221> CDS  
 <222> (125)..(1399)

<220>  
 <223> Description of Unknown Organism:Murine NR6.2

<400> 14  
 ggcacgagct tcgctgtccg cgcccagtgga cgcgcggtgcg gacccgagcc ccaatctgca 60  
 ccccgagac tcgccccgcg cccataccgg cggtgcagtc accgcccgtt gcgcgccacc 120  
 ccca atg ccc gcg ggt cgc ccg ggc ccc gtc gcc caa tcc gcg cgg cgg 169  
 Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg  
 1 5 10 15  
 ccg ccg cgg ccg ctg tcc tcg ctg tgg tcg cct ctg ttg ctc tgt gtc 217  
 Pro Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val  
 20 25 30  
 ctc ggg gtg cct cgg ggc gga tcg gga gcc cac aca gct gta atc agc 265  
 Leu Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser  
 35 40 45  
 ccc cag gac ccc acc ctt ctc atc ggc tcc tcc ctg caa gct acc tgc 313  
 Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys  
 50 55 60  
 tct ata cat gga gac aca cct ggg gcc acc gct gag ggg ctc tac tgg 361  
 Ser Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp  
 65 70 75  
 acc ctc aat ggt cgc cgc ctg ccc tct gag ctg tcc cgc ctc ctt aac 409  
 Thr Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn  
 80 85 90 95

acc tcc acc ctg gcc ctg gcc ctg gct aac ctt aat ggg tcc agg cag	457
Thr Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln	
100 105 110	
cag tca gga gac aat ctg gtg tgt cac gcc cga gac ggc agc att ctg	505
Gln Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu	
115 120 125	
gct ggc tcc tgc ctc tat gtt ggc ttg ccc cct gag aag ccc ttt aac	553
Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn	
130 135 140	
atc agc tgc tgg tcc cgg aac atg aag gat ctc acg tgc cgc tgg aca	601
Ile Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr	
145 150 155	
ccg ggt gca cac ggg gag aca ttc tta cat acc aac tac tcc ctc aag	649
Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys	
160 165 170 175	
tac aag ctg agg tgg tac ggt cag gat aac aca tgt gag gag tac cac	697
Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His	
180 185 190	
act gtg ggc cct cac tca tgc cat atc ccc aag gac ctg gcc ctc ttc	745
Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe	
195 200 205	
act ccc tat gag atc tgg gtg gaa gcc acc aat cgc cta ggc tca gca	793
Thr Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala	
210 215 220	
aga tct gat gtc ctc aca ctg gat gtc ctg gac gtg gtg acc acg gac	841
Arg Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp	
225 230 235	
ccc cca ccc gac gtg cac gtg agc cgc gtt ggg ggc ctg gag gac cag	889
Pro Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln	
240 245 250 255	
ctg agt gtg cgc tgg gtc tca cca cca gct ctc aag gat ttc ctc ttc	937
Leu Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe	
260 265 270	
caa gcc aag tac cag atc cgc tac cgc gtg gag gac agc gtg gac tgg	985
Gln Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp	
275 280 285	
aag gtg gtg gat gac gtc agc aac cag acc tcc tgc cgt ctc gcg ggc	1033
Lys Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly	
290 295 300	
ctg aag ccc ggc acc gtt tac ttc gtc caa gtg cgt tgt aac cca ttc	1081
Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe	
305 310 315	
ggg atc tat ggg tcg aaa aag gcg gga atc tgg agc gag tgg agc cac	1129

Gly	Ile	Tyr	Gly	Ser	Lys	Lys	Ala	Gly	Ile	Trp	Ser	Glu	Trp	Ser	His	
320					325					330					335	
ccc	acc	gct	gcc	tcc	acc	cct	cga	agt	gag	cgc	ccg	ggc	ccg	ggc	ggc	1177
Pro	Thr	Ala	Ala	Ser	Thr	Pro	Arg	Ser	Glu	Arg	Pro	Gly	Pro	Gly	Gly	
				340					345					350		
ggg	gtg	tgc	gag	ccg	cgg	ggc	ggc	gag	ccc	agc	tcg	ggc	ccg	gtg	cgg	1225
Gly	Val	Cys	Glu	Pro	Arg	Gly	Gly	Glu	Pro	Ser	Ser	Gly	Pro	Val	Arg	
			355					360					365			
cgc	gag	ctc	aag	cag	ttc	ctc	ggc	tgg	ctc	aag	aag	cac	gca	tac	tgc	1273
Arg	Glu	Leu	Lys	Gln	Phe	Leu	Gly	Trp	Leu	Lys	Lys	His	Ala	Tyr	Cys	
		370					375					380				
tcg	aac	ctt	agt	ttc	cgc	ctg	tac	gac	cag	tgg	cgt	gct	tgg	atg	cag	1321
Ser	Asn	Leu	Ser	Phe	Arg	Leu	Tyr	Asp	Gln	Trp	Arg	Ala	Trp	Met	Gln	
	385					390					395					
aag	tca	cac	aag	acc	cga	aac	cag	gac	gag	ggg	atc	ctg	cct	tcg	ggc	1369
Lys	Ser	His	Lys	Thr	Arg	Asn	Gln	Asp	Glu	Gly	Ile	Leu	Pro	Ser	Gly	
400					405					410					415	
aga	cgg	ggt	gcg	gcg	aga	ggt	cct	gcc	ggt	taaactctaa	ggataggcca					1419
Arg	Arg	Gly	Ala	Ala	Arg	Gly	Pro	Ala	Gly							
				420					425							
tcctcctgct	gggtcagacc	tggaggctca	cctgaattgg	agcccctctg	taccatctgg											1479
gcaacaaaga	aacctaccag	aggctggggc	acaatgagct	cccacaacca	cagcttttgg											1539
ccacatgatg	gtcacacttg	gatatacccc	agtgtgggta	aggttggggg	attgcagggc											1599
ctcccaacaa	tctctttaaa	taaataaagg	agttgttcag	gtaaaaaaaa	aaaaaaaaaa											1659
aaaaaaaaaa	aaaa															1673

<210> 15  
 <211> 425  
 <212> PRT  
 <213> Unknown

<220>

<223> Description of Unknown Organism: Murine NR6.2

<400> 15

Met	Pro	Ala	Gly	Arg	Pro	Gly	Pro	Val	Ala	Gln	Ser	Ala	Arg	Arg	Pro
1				5					10					15	
Pro	Arg	Pro	Leu	Ser	Ser	Leu	Trp	Ser	Pro	Leu	Leu	Leu	Cys	Val	Leu
			20					25					30		
Gly	Val	Pro	Arg	Gly	Gly	Ser	Gly	Ala	His	Thr	Ala	Val	Ile	Ser	Pro
		35					40					45			
Gln	Asp	Pro	Thr	Leu	Leu	Ile	Gly	Ser	Ser	Leu	Gln	Ala	Thr	Cys	Ser

50					55					60					
Ile 65	His	Gly	Asp	Thr	Pro 70	Gly	Ala	Thr	Ala	Glu 75	Gly	Leu	Tyr	Trp	Thr 80
Leu	Asn	Gly	Arg	Arg 85	Leu	Pro	Ser	Glu	Leu 90	Ser	Arg	Leu	Leu	Asn 95	Thr
Ser	Thr	Leu	Ala 100	Leu	Ala	Leu	Ala	Asn 105	Leu	Asn	Gly	Ser	Arg 110	Gln	Gln
Ser	Gly	Asp 115	Asn	Leu	Val	Cys	His 120	Ala	Arg	Asp	Gly	Ser 125	Ile	Leu	Ala
Gly 130	Ser	Cys	Leu	Tyr	Val	Gly 135	Leu	Pro	Pro	Glu	Lys 140	Pro	Phe	Asn	Ile
Ser 145	Cys	Trp	Ser	Arg	Asn 150	Met	Lys	Asp	Leu	Thr 155	Cys	Arg	Trp	Thr	Pro 160
Gly	Ala	His	Gly	Glu 165	Thr	Phe	Leu	His	Thr 170	Asn	Tyr	Ser	Leu	Lys 175	Tyr
Lys	Leu	Arg	Trp 180	Tyr	Gly	Gln	Asp	Asn 185	Thr	Cys	Glu	Glu	Tyr 190	His	Thr
Val	Gly 195	Pro	His	Ser	Cys	His	Ile 200	Pro	Lys	Asp	Leu	Ala 205	Leu	Phe	Thr
Pro 210	Tyr	Glu	Ile	Trp	Val	Glu 215	Ala	Thr	Asn	Arg	Leu 220	Gly	Ser	Ala	Arg
Ser 225	Asp	Val	Leu	Thr	Leu 230	Asp	Val	Leu	Asp	Val 235	Val	Thr	Thr	Asp	Pro 240
Pro	Pro	Asp	Val	His 245	Val	Ser	Arg	Val	Gly 250	Gly	Leu	Glu	Asp	Gln 255	Leu
Ser	Val	Arg	Trp 260	Val	Ser	Pro	Pro	Ala 265	Leu	Lys	Asp	Phe	Leu 270	Phe	Gln
Ala	Lys 275	Tyr	Gln	Ile	Arg	Tyr	Arg 280	Val	Glu	Asp	Ser	Val 285	Asp	Trp	Lys
Val 290	Val	Asp	Asp	Val	Ser	Asn 295	Gln	Thr	Ser	Cys	Arg 300	Leu	Ala	Gly	Leu
Lys 305	Pro	Gly	Thr	Val	Tyr 310	Phe	Val	Gln	Val	Arg 315	Cys	Asn	Pro	Phe	Gly 320
Ile	Tyr	Gly	Ser	Lys 325	Lys	Ala	Gly	Ile	Trp 330	Ser	Glu	Trp	Ser	His 335	Pro
Thr	Ala	Ala	Ser 340	Thr	Pro	Arg	Ser	Glu 345	Arg	Pro	Gly	Pro	Gly 350	Gly	Gly
Val	Cys	Glu	Pro	Arg	Gly	Gly	Glu	Pro	Ser	Ser	Gly	Pro	Val	Arg	Arg

355		360		365
Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser				
370		375		380
Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys				
385		390		395
Ser His Lys Thr Arg Asn Gln Asp Glu Gly Ile Leu Pro Ser Gly Arg				
	405		410	415
Arg Gly Ala Ala Arg Gly Pro Ala Gly				
	420		425	

<210> 16  
 <211> 938  
 <212> DNA  
 <213> Unknown

<220>  
 <221> CDS  
 <222> (1)..(465)

<220>  
 <223> Description of Unknown Organism:Murine NR6.3

<400> 16	
ggc acc gtt tac ttc gtc caa gtg cgt tgt aac cca ttc ggg atc tat	48
Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr	
1 5 10 15	
ggg tcg aaa aag gcg gga atc tgg agc gag tgg agc cac ccc acc gct	96
Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro Thr Ala	
20 25 30	
gcc tcc acc cct cga agt gag cgc ccg ggc ccg ggc ggc ggg gtg tgc	144
Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Gly Val Cys	
35 40 45	
gag ccg cgg ggc ggc gag ccc agc tcg ggc ccg gtg cgg cgc gag ctc	192
Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg Glu Leu	
50 55 60	
aag cag ttc ctc ggc tgg ctc aag aag cac gca tac tgc tcg aac ctt	240
Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser Asn Leu	
65 70 75 80	
agt ttc cgc ctg tac gac cag tgg cgt gct tgg atg cag aag tca cac	288
Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys Ser His	
85 90 95	
aag acc cga aac cag gta gga aag ttg ggg gag gct tgc gtg ggg ggt	336
Lys Thr Arg Asn Gln Val Gly Lys Leu Gly Glu Ala Cys Val Gly Gly	
100 105 110	
aaa gga gca gag gaa gag aga gac ccg ggt gag cag cct cca caa cac	384

Lys Gly Ala Glu Glu Glu Arg Asp Pro Gly Glu Gln Pro Pro Gln His  
 115 120 125  
 cgc act ctt ctt tcc aag cac agg acg agg gga tcc tgc cct cgg gca 432  
 Arg Thr Leu Leu Ser Lys His Arg Thr Arg Gly Ser Cys Pro Arg Ala  
 130 135 140  
 gac ggg gtg cgg cga gag gta agg ggg tct ggg tgagtggggc ctacagcagt 485  
 Asp Gly Val Arg Arg Glu Val Arg Gly Ser Gly  
 145 150 155  
 ctagatgagg ccctttcccc tccttcggtg ttgctcaaag ggatctctta gtgctcattt 545  
 caccactgc aaagagcccc aggttttact gcatcatcaa gttgctgaag ggtccaggct 605  
 taatgtggcc tcttttctgc cctcagggtcc tgccggctaa actctaagga taggccatcc 665  
 tcctgctggg tcagacctgg aggcacacct gaattggagc ccctctgtac ctatctgggc 725  
 aacaaagaaa cctaccatga ggctggggca caatgagctc ccacaaccac agctttggtc 785  
 cacatgatgg tcacacttgg atatacccca gtgtgggtaa ggttggggta ttgcagggcc 845  
 tcccaacaat ctctttaaat aaataaagga gttgttcagg taaaaaaaaa aaaaaaaaaa 905  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 938

<210> 17  
 <211> 155  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Description of Unknown Organism: Murine NR6.3

<400> 17  
 Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr  
 1 5 10 15  
 Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro Thr Ala  
 20 25 30  
 Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Val Cys  
 35 40 45  
 Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg Glu Leu  
 50 55 60  
 Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser Asn Leu  
 65 70 75 80  
 Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys Ser His  
 85 90 95  
 Lys Thr Arg Asn Gln Val Gly Lys Leu Gly Glu Ala Cys Val Gly Gly  
 100 105 110

Lys Gly Ala Glu Glu Glu Arg Asp Pro Gly Glu Gln Pro Pro Gln His  
115 120 125

Arg Thr Leu Leu Ser Lys His Arg Thr Arg Gly Ser Cys Pro Arg Ala  
130 135 140

Asp Gly Val Arg Arg Glu Val Arg Gly Ser Gly  
145 150 155

<210> 18  
<211> 834  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> CDS  
<222> (1)..(834)

<220>  
<223> Description of Artificial Sequence: Nucleotide  
sequence of products generated by 5' RACE of brain  
cDNA using NR6 specific primers

<400> 18  
ccc acc ctt ctc atc ggc tcc tcc ctg caa gct acc tgc tct ata cat 48  
Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser Ile His  
1 5 10 15

gga gac aca cct ggg gcc acc gct gag ggg ctc tac tgg acc ctc aat 96  
Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr Leu Asn  
20 25 30

ggt cgc cgc ctg ccc tct gag ctg tcc cgc ctc ctt aac acc tcc acc 144  
Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr Ser Thr  
35 40 45

ctg gcc ctg gcc ctg gct aac ctt aat ggg tcc agg cag cag tca gga 192  
Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln Ser Gly  
50 55 60

gac aat ctg gtg tgt cac gcc cga gac ggc agc att ctg gct ggc tcc 240  
Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala Gly Ser  
65 70 75 80

tgc ctc tat gtt ggc ttg ccc cct gag aag ccc ttt aac atc agc tgc 288  
Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile Ser Cys  
85 90 95

tgg tcc cgg aac atg aag gat ctc acg tgc cgc tgg aca ccg ggt gca 336  
Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro Gly Ala  
100 105 110

cac ggg gag aca ttc tta cat acc aac tac tcc ctc aag tac aag ctg 384  
His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr Lys Leu  
115 120 125

agg tgg tac ggt cag gat aac aca tgt gag gag tac cac act gtg ggg	432
Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr Val Gly	
130 135 140	
ccc cac tca tgc cat atc ccc aag gac ctg gcc ctc ttc act ccc tat	480
Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr Pro Tyr	
145 150 155 160	
gag atc tgg gtg gaa gcc acc aat cgc cta ggc tca gca aga tct gat	528
Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg Ser Asp	
165 170 175	
gtc ctc aca ctg gat gtc ctg gac gtg gtg acc acg gac ccc cca ccc	576
Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro Pro Pro	
180 185 190	
gac gtg cac gtg agc cgc gtt ggg ggc ctg gag gac cag ctg agt gtg	624
Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu Ser Val	
195 200 205	
cgc tgg gtc tca cca cca gct ctc aag gat ttc ctc ttc caa gcc aag	672
Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln Ala Lys	
210 215 220	
tac cag atc cgc tac cgc gtg gag gac agc gtg gac tgg aag gtg gtg	720
Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys Val Val	
225 230 235 240	
gat gac gtc agc aac cag acc tcc tgc cgt ctc gcg ggc ctg aag ccc	768
Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu Lys Pro	
245 250 255	
ggc acc gtt tac ttc gtc caa gtg cgt tgt aac cca ttc ggg atc tat	816
Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr	
260 265 270	
ggg tcg aaa aag gcg gga	834
Gly Ser Lys Lys Ala Gly	
275	

<210> 19

<211> 278

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Haemopoietin receptor

<400> 19

Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser Ile His
1 5 10 15

Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr Leu Asn
20 25 30

Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr Ser Thr
---



35					40					45					
Leu	Ala	Leu	Ala	Leu	Ala	Asn	Leu	Asn	Gly	Ser	Arg	Gln	Gln	Ser	Gly
	50					55					60				
Asp	Asn	Leu	Val	Cys	His	Ala	Arg	Asp	Gly	Ser	Ile	Leu	Ala	Gly	Ser
65					70					75					80
Cys	Leu	Tyr	Val	Gly	Leu	Pro	Pro	Glu	Lys	Pro	Phe	Asn	Ile	Ser	Cys
				85					90					95	
Trp	Ser	Arg	Asn	Met	Lys	Asp	Leu	Thr	Cys	Arg	Trp	Thr	Pro	Gly	Ala
			100					105					110		
His	Gly	Glu	Thr	Phe	Leu	His	Thr	Asn	Tyr	Ser	Leu	Lys	Tyr	Lys	Leu
		115					120					125			
Arg	Trp	Tyr	Gly	Gln	Asp	Asn	Thr	Cys	Glu	Glu	Tyr	His	Thr	Val	Gly
	130					135					140				
Pro	His	Ser	Cys	His	Ile	Pro	Lys	Asp	Leu	Ala	Leu	Phe	Thr	Pro	Tyr
145					150					155					160
Glu	Ile	Trp	Val	Glu	Ala	Thr	Asn	Arg	Leu	Gly	Ser	Ala	Arg	Ser	Asp
				165					170					175	
Val	Leu	Thr	Leu	Asp	Val	Leu	Asp	Val	Val	Thr	Thr	Asp	Pro	Pro	Pro
			180					185					190		
Asp	Val	His	Val	Ser	Arg	Val	Gly	Gly	Leu	Glu	Asp	Gln	Leu	Ser	Val
		195					200					205			
Arg	Trp	Val	Ser	Pro	Pro	Ala	Leu	Lys	Asp	Phe	Leu	Phe	Gln	Ala	Lys
	210					215					220				
Tyr	Gln	Ile	Arg	Tyr	Arg	Val	Glu	Asp	Ser	Val	Asp	Trp	Lys	Val	Val
225					230					235					240
Asp	Asp	Val	Ser	Asn	Gln	Thr	Ser	Cys	Arg	Leu	Ala	Gly	Leu	Lys	Pro
				245					250					255	
Gly	Thr	Val	Tyr	Phe	Val	Gln	Val	Arg	Cys	Asn	Pro	Phe	Gly	Ile	Tyr
			260					265					270		
Gly	Ser	Lys	Lys	Ala	Gly										
		275													

<210> 20  
 <211> 143  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <221> CDS  
 <222> (105)..(143)

<220>

<223> Description of Artificial Sequence:Nucleotide  
sequence unique to 5' RACE of brain cDNA

<400> 20

ggcatgaagg cttaggggtgg ggatcggtag gacccatgca cccagagaaa gggactgggtg 60  
gcaactttca aactctctgg ggaaggaaga agggctgaaa gagg atg aac ggg ctc 116  
Met Asn Gly Leu  
1

aga cac agc tgt aat cag ccc cca gga 143  
Arg His Ser Cys Asn Gln Pro Pro Gly  
5 10

<210> 21

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino Acid Sequence encoded  
by Nucleotide sequence unique to 5' RACE of brain cDNA

<400> 21

Met Asn Gly Leu Arg His Ser Cys Asn Gln Pro Pro Gly  
1 5 10

<210> 22

<211> 1930

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:Murine NR6

<400> 22

ggcacgagct tcgctgtccg cgcccagtga cgcgcggtgcg gacccgagcc ccaatctgca 60  
ccccgcagac tcgccccgcg cccataccgg cggtgcagtc accgcccgtt gcgcgccacc 120  
cccaatgccc gcggggtcgc cgggccccgt cgcccaatcc gcgcggcggc gcgcgcggcc 180  
gctgtcctcg ctgtggtcgc ctctgttgct ctgtgtcctc ggggtgcctc ggggcggatc 240  
gggagcccac acagctgtaa tcagcccccga ggaccccacc cttctcatcg gctcctccct 300  
gcaagctacc tgctctatac atggagacac acctggggcc accgctgagg ggctctactg 360  
gaccctcaat ggtgcgcgcc tgccctctga gctgtccgcg ctccttaaca cctccaccct 420  
ggccctggcc ctggctaacc ttaatgggtc caggcagcag tcaggagaca atctggtgtg 480  
tcacgcccga gacggcagca ttctgggtgg ctctgcctc tatgttggtg tgccccctga 540

gaagcccttt aacatcagct gctggtcccg gaacatgaag gatctcacgt gccgctggac 600  
 accgggtgca cacggggaga cattcttaca taccaactac tccctcaagt acaagctgag 660  
 gtggtacggt caggataaca catgtgagga gtaccacact gtgggccctc actcatgcca 720  
 tatccccaag gacctggccc tcttcactcc ctatgagatc tgggtggaag ccaccaatcg 780  
 cctaggetca gcaagatctg atgtcctcac actggatgtc ctggacgtgg tgaccacgga 840  
 cccccaccc gacgtgcacg tgagccgctg tgggggctg gaggaccagc tgagtgtgcg 900  
 ctgggtctca ccaccagctc tcaaggattt cctcttccaa gccaaagtacc agatccgcta 960  
 ccgctgggag gacagcgtgg actggaaggt ggtggatgac gtcagcaacc agacctcctg 1020  
 ccgtctcgcg ggcctgaagc ccggcaccgt ttacttcgtc caagtgcgtt gtaaccatt 1080  
 cgggatctat gggctgaaaa aggcgggaat ctggagcgag tggagccacc ccaccgctgc 1140  
 ctccaccct cgaagtgagc gcccgggccc gggcggcggg gtgtgcgagc cgcggggcgg 1200  
 cgagcccagc tcgggcccgg tgcggcgcg a gctcaagcag ttcctcggct ggctcaagaa 1260  
 gcacgcatac tgctcgaacc ttagtttccg cctgtacgac cagtggcgtg cttggatgca 1320  
 gaagtcacac aagaccgaa accaggtagg aaagttgggg gaggcttgcg tggggggtaa 1380  
 aggagcagag gaagagagag acccgggtga gcagcctcca caacaccgca ctcttctttc 1440  
 caagcacagg acgaggggat cctgccctcg ggcagacggg gtgcggcgag aggtaagggg 1500  
 gtctgggtga gtggggccta cagcagtcta gatgaggccc tttcccctcc ttcggtgttg 1560  
 ctcaaaggga tctcttagtg ctcatctcac ccactgcaaa gagccccagg ttttactgca 1620  
 tcatcaagtt gctgaagggt ccaggcttaa tgtggcctct tttctgccct caggtcctgc 1680  
 cggctaaact ctaaggatag gccatcctcc tgctgggtca gacctggagg ctcacctgaa 1740  
 ttggagcccc tctgtaccta tctgggcaac aaagaaacct accatgaggc tggggcaciaa 1800  
 tgagctccca caaccacagc tttggtccac atgatgggtca cacttgata taccacagt 1860  
 tgggtaaggt tggggtattg cagggcctcc caacaatctc tttaaataaa taaaggagtt 1920  
 gttcaggtaa 1930

<210> 23

<211> 560

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR product for human NR6

<400> 23  
tccaggcagc ggtcggggga caacctcgtg tgccacgccc gtgacggcag catcctggct 60  
ggctcctgcc tctatgttgg cctgccccca gagaaacccg tcaacatcag ctgctgggtcc 120  
aagaacatga aggacttgac ctgccgctgg acgccagggg cccacgggga gaccttcctc 180  
cacaccaact actccctcaa gtacaagctt aggtgggtatg gccaggacaa cacatgtgag 240  
gagtaccaca cagtgggggc cactcctgc cacatcccca aggacctggc tctctttacg 300  
ccctatgaga tctgggtgga ggccaccaac cgctgggct ctgcccgctc cgatgtactc 360  
acgctggata tcctggatgt ggtgaccacg gacccccgc ccgacgtgca cgtgagccgc 420  
gtcggggggc tggaggacca gctgagcgtg cgctgggtgt cgccaccgc cctcaaggat 480  
ttcctttttc aagccaaata ccagatccgc taccgagtgg aggacagtgt ggaatggaag 540  
gtggtggacg atgtgagcaa 560

<210> 24  
<211> 1391  
<212> DNA  
<213> Unknown

<220>  
<221> CDS  
<222> (1)..(1050)

<220>  
<223> Description of Unknown Organism:Nucleotide  
sequence of clone HFK-66 encoding human NR6

<400> 24  
acc ctc aac ggg cgc cgc ctg ccc cct gag ctc tcc cgt gta ctc aac 48  
Thr Leu Asn Gly Arg Arg Leu Pro Pro Glu Leu Ser Arg Val Leu Asn  
1 5 10 15  
gcc tcc acc ttg gct ctg gcc ctg gcc aac ctc aat ggg tcc agg cag 96  
Ala Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln  
20 25 30  
cgg tcg ggg gac aac ctc gtg tgc cac gcc cgt gac ggc agc atc ctg 144  
Arg Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu  
35 40 45  
gct ggc tcc tgc ctc tat gtt ggc ctg ccc cca gag aaa ccc gtc aac 192  
Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Val Asn  
50 55 60  
atc agc tgc tgg tcc aag aac atg aag gac ttg acc tgc cgc tgg acg 240  
Ile Ser Cys Trp Ser Lys Asn Met Lys Asp Leu Thr Cys Arg Trp Thr  
65 70 75 80  
cca ggg gcc cac ggg gag acc ttc ctc cac acc aac tac tcc ctc aag 288

Pro	Gly	Ala	His	Gly	Glu	Thr	Phe	Leu	His	Thr	Asn	Tyr	Ser	Leu	Lys	
				85					90					95		
tac	aag	ctt	agg	tgg	tat	ggc	cag	gac	aac	aca	tgt	gag	gag	tac	cac	336
Tyr	Lys	Leu	Arg	Trp	Tyr	Gly	Gln	Asp	Asn	Thr	Cys	Glu	Glu	Tyr	His	
			100					105					110			
aca	gtg	ggg	ccc	cac	tcc	tgc	cac	atc	ccc	aag	gac	ctg	gct	ctc	ttt	384
Thr	Val	Gly	Pro	His	Ser	Cys	His	Ile	Pro	Lys	Asp	Leu	Ala	Leu	Phe	
		115					120					125				
acg	ccc	tat	gag	atc	tgg	gtg	gag	gcc	acc	aac	cgc	ctg	ggc	tct	gcc	432
Thr	Pro	Tyr	Glu	Ile	Trp	Val	Glu	Ala	Thr	Asn	Arg	Leu	Gly	Ser	Ala	
	130					135					140					
cgc	tcc	gat	gta	ctc	acg	ctg	gat	atc	ctg	gat	gtg	gtg	acc	acg	gac	480
Arg	Ser	Asp	Val	Leu	Thr	Leu	Asp	Ile	Leu	Asp	Val	Val	Thr	Thr	Asp	
145					150					155					160	
ccc	ccg	ccc	gac	gtg	cac	gtg	agc	cgc	gtc	ggg	ggc	ctg	gag	gac	cag	528
Pro	Pro	Pro	Asp	Val	His	Val	Ser	Arg	Val	Gly	Gly	Leu	Glu	Asp	Gln	
				165					170					175		
ctg	agc	gtg	cgc	tgg	gtg	tcg	cca	ccc	gcc	ctc	aag	gat	ttc	ctc	ttt	576
Leu	Ser	Val	Arg	Trp	Val	Ser	Pro	Pro	Ala	Leu	Lys	Asp	Phe	Leu	Phe	
			180					185					190			
caa	gcc	aaa	tac	cag	atc	cgc	tac	cga	gtg	gag	gac	agt	gtg	gac	tgg	624
Gln	Ala	Lys	Tyr	Gln	Ile	Arg	Tyr	Arg	Val	Glu	Asp	Ser	Val	Asp	Trp	
		195					200					205				
aag	gtg	gtg	gac	gat	gtg	agc	aac	cag	acc	tcc	tgc	cgc	ctg	gcc	ggc	672
Lys	Val	Val	Asp	Asp	Val	Ser	Asn	Gln	Thr	Ser	Cys	Arg	Leu	Ala	Gly	
	210					215					220					
ctg	aaa	ccc	ggc	acc	gtg	tac	ttc	gtg	caa	gtg	cgc	tgc	aac	ccc	ttt	720
Leu	Lys	Pro	Gly	Thr	Val	Tyr	Phe	Val	Gln	Val	Arg	Cys	Asn	Pro	Phe	
225					230					235					240	
ggc	atc	tat	ggc	tcc	aag	aaa	gcc	ggg	atc	tgg	agt	gag	tgg	agc	cac	768
Gly	Ile	Tyr	Gly	Ser	Lys	Lys	Ala	Gly	Ile	Trp	Ser	Glu	Trp	Ser	His	
				245					250					255		
ccc	aca	gcc	gcc	tcc	act	ccc	cgc	agt	gag	cgc	ccg	ggc	ccg	ggc	ggc	816
Pro	Thr	Ala	Ala	Ser	Thr	Pro	Arg	Ser	Glu	Arg	Pro	Gly	Pro	Gly	Gly	
				260				265					270			
ggg	gcg	tgc	gaa	ccg	cgg	ggc	gga	gag	ccg	agc	tcg	ggg	ccg	gtg	cgg	864
Gly	Ala	Cys	Glu	Pro	Arg	Gly	Gly	Glu	Pro	Ser	Ser	Gly	Pro	Val	Arg	
		275					280					285				
cgc	gag	ctc	aag	cag	ttc	ctg	ggc	tgg	ctc	aag	aag	cac	gcg	tac	tgc	912
Arg	Glu	Leu	Lys	Gln	Phe	Leu	Gly	Trp	Leu	Lys	Lys	His	Ala	Tyr	Cys	
	290					295					300					
tcc	aac	ctc	agc	ttc	cgc	ctc	tac	gac	cag	tgg	cga	gcc	tgg	atg	cag	960
Ser	Asn	Leu	Ser	Phe	Arg	Leu	Tyr	Asp	Gln	Trp	Arg	Ala	Trp	Met	Gln	

305				310				315				320				
aag	tcg	cac	aag	acc	cgc	aac	cag	cac	agg	acg	agg	gga	tcc	tgc	cct	1008
Lys	Ser	His	Lys	Thr	Arg	Asn	Gln	His	Arg	Thr	Arg	Gly	Ser	Cys	Pro	
				325					330					335		
cgg	gca	gac	ggg	gca	cgg	cga	gag	gtc	ctg	cca	gat	aag	ctg			1050
Arg	Ala	Asp	Gly	Ala	Arg	Arg	Glu	Val	Leu	Pro	Asp	Lys	Leu			
			340					345					350			
taggggctca ggccaccctc cctgccacgt ggagacgcag aggccgaacc caaactgggg 1110																
ccacctctgt accctcactt cagggcacct gagcccctca gcaggagctg ggggtggcccc 1170																
tgagctccaa cggccataac agctctgact cccacgtgag gccacctttg ggtgcacccc 1230																
agtgggtgtg tgtgtgtgtg tgagggttgg ttgagttgcc tagaaccctt gccagggctg 1290																
ggggtgagaa ggggagtcac tactccccat tacctagggc ccctccaaaa gagtcctttt 1350																
aaataaatga gctattttaag tgcaaaaaaaaa aaaaaaaaaa a 1391																

130	135	140
Arg Ser Asp Val Leu Thr Leu Asp Ile Leu Asp Val Val Thr Thr Asp 145 150 155 160		
Pro Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln 165 170 175		
Leu Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe 180 185 190		
Gln Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp 195 200 205		
Lys Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly 210 215 220		
Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe 225 230 235 240		
Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His 245 250 255		
Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly 260 265 270		
Gly Ala Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg 275 280 285		
Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys 290 295 300		
Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln 305 310 315 320		
Lys Ser His Lys Thr Arg Asn Gln His Arg Thr Arg Gly Ser Cys Pro 325 330 335		
Arg Ala Asp Gly Ala Arg Arg Glu Val Leu Pro Asp Lys Leu 340 345 350		

<210> 26

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:UP1  
Oligonucleotide

<400> 26

tccaggcagc ggctcggggga caac

24

<210> 27

<211> 24

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:LP1  
Oligonucleotide

<400> 27  
ttgctcacat cgtccaccac cttc

24

<210> 28  
<211> 6663  
<212> DNA  
<213> Unknown

<220>  
<223> Description of Unknown Organism:Murine NR6 gene

<400> 28  
cccagaactc ttggacgctg aggcaggagg attcccaagt ttcaagacag tgtgttttcta 60  
ggtaatgaga ccctgtcaag aaaagaaaag aaataaagag acaagaaaat gtttataggc 120  
tgtgagacag cttggtgggt aaggggcact tgcctccaat caagatgacc tcagcccat 180  
ccctaggaat ccatggtaga aggagaaagc aaactcgcag ctgctgacct ccatacatgt 240  
gctccaatgt gcacacacac agggagacat aatcaattaa taggatgtat ttgcttagat 300  
ttgagtaggc atttatgact gatgttttaa aatttttatt tgattttatg aaaatatacc 360  
tgtttgtatt tggtttggtt tggtttgagt tttgtttatt tgagacaggg cttctctgtg 420  
tagtcctggc tgtccttgga actcactctg tagaccaggc tggccttgaa ctcagaaatc 480  
cgctgcttg tgcctcccaa gtgcttagat taaagggtgtg cactgccatt cagcaaaatt 540  
gcatacttta accccagtat ttgggaggca gaggcagact aatgtgtgaa ttccaggcta 600  
gccaaggata cagagtgaga ccctattctt accctcccc cccaaaacc caaatgtat 660  
tttggtgctt tgtatgtaca tgtgtgttgc agcacgtaaa tgtccaagga caacttgtag 720  
aagttctctc cgttcacagt ctaagtcctg aattcaaact aaggtcctca ggcttagcca 780  
cagtcttctt tatgtactga gccatttcac tggccctgga ttgactgatg aattaatttt 840  
tgagataagg tctctttagt ctctagctag gctcaaacta tgaactccca aggtcatctt 900  
gagctgcttg tactcttgct tccaccccaa gtggtggaat gatactcagg cagcacttct 960  
ctggggaagg ggctggcctt ggccttgatt ttgttgctc agcttcaatg agtgcttggg 1020  
tctcgttgtt tcttttcttt atctgtgaaa tgggtgaaca cctgttcaag acttctgac 1080  
tcttgaaaca tccaggcagg gtgagggact tgaagtgggc tcatcccatg cctaacaaag 1140



tgtcgtcttt gaccccagac acagctgtaa tcagcccccga ggaccccacc cttctcatcg 1200  
 gctcctccct gcaagctacc tgctctatac atggagacac acctgggggc accgctgagg 1260  
 ggctctactg gaccttcaat ggtcgccgcc tgccctctga gctgtcccgc ctccttaaca 1320  
 cctccaccct ggccctggcc ctggctaacc ttaatgggtc caggcagcag tcaggagaca 1380  
 atctgggtgtg tcacgcccga gacggcagca ttctgggtgg ctctgcctc tatgttggct 1440  
 gtaagtgggg cccagacac tcagagatag atgggggttg gcaatgacag atttagagcc 1500  
 tgggtcttct gtccctggggc agagccatgg gctctcactt gcatgcaggc atggtcatac 1560  
 ccagcacagg cattgcaact ctagggacag ctgtgggtgc actgtcccct gtgtacccca 1620  
 cagctttaga aaagctgtca tgttttcctt gtagtgcccc ctgagaagcc ctttaacatc 1680  
 agctgctggc cccggaacat gaaggatctc acgtgccgct ggacaccggg tgcacacggg 1740  
 gagacattct tacataccaa ctactccctc aagtacaagc tgaggttggc acccagccaa 1800  
 gccttgctgt gtgacttctg gcaatactta cttctctga tcaaataatgt tcctgtttat 1860  
 gaactcaaaa gggactctcg caccctccaca ggtgggtacgg tcaggataac acatgtgagg 1920  
 agtaccacac tgtgggccct cactcatgcc atatcccca ggacctggcc ctcttcactc 1980  
 cctatgagat ctgggtggaa gccaccaatc gcctaggctc agcaagatct gatgtcctca 2040  
 cactggatgt cctggacgtg ggtgagcccc cagtgtccac ctgtgttctg ccctagacct 2100  
 tataggcgcc ctccccccca tccccccaga ctttttggtt cttctagagg tcttagccac 2160  
 agccacggtg gttgcaggac agtgggtggt cataacttaa tgcaaagact tcccccaag 2220  
 acagtcaaga tttttccctt cccaccccc aacacacaca tacacacaca ctctgcagag 2280  
 aacacctggc ctgaccaccc tccctctcta cagcccaggt gttcagaagg gagtcctagg 2340  
 ggactgagag gaggcgcccc ggtctgaagg cgccccagga agccgaggcc ttgagctggg 2400  
 ggggggggcg aggggtggag gcacgaactg gatgatccct gagcacaact gggcctaatac 2460  
 taattagggc gttcccagcc caaagcagcc tgggccatth aacccttcaa gtgcctcact 2520  
 gaagactcag gggagagatc agcttgact ctctccatgg tccccagga gggttcctgg 2580  
 gtgcccctgg ctcatccca catccagagg ttttgtgtct tcctggcatc taaccctcag 2640  
 ttgtgctctg tggtggcac agctgccccg tggaggctct tggtaatgta caaggcatca 2700  
 gaggtggaca tgggatgggg atacataggg atggagccaa atagcacctc aagggtgggg 2760  
 gatatacaat aaagcttgtc accctgacgc tcagaaagcc tactcatgat gatcacaatt 2820  
 gttgacatca ctctgggaca tgtagtgaga ccctagctca aaacacagac agtagcttta 2880

agagtcagct tgtgacttaa tactggaact cagggcctaa taggtgctgg gtgatgctcg 2940  
 cctcactccc tgtttagaga gatctctgcg ctaatctcca cccagctgg gtgggctgct 3000  
 ctgtcccctt gagggcagga atgtgtgtct tccatcagag ataggacccg tggtagcagc 3060  
 aactgctgct ggctgtttct ggaatattaa atgacagtaa tctatcaggc ctgggtgagt 3120  
 agctaacagg ggtgggggcg tggctctgaa aacgcagata gggcatagg agccactgca 3180  
 gcctagatta caccactggg tgttctgtca ctaggccatt ctcaccaagc agtcctcaga 3240  
 actgggagca ctgttgccag catttaatgc cagcatttaa tgccagcatt aggggaggca 3300  
 gaggcagaag gatctctctg agttcaaggc catcctgaat ttacataaag agctccaggc 3360  
 cagccagggt gcgcagtaaa accttgtctc aaaaaacaaa gcatctttag tgaccaggct 3420  
 tgctccacc ccagtgacca cggaccccc acccgacgtg cacgtgagcc gcgttggggg 3480  
 cctggaggac cagctgagtg tgcgctgggt ctcaccacca gctctcaagg atttctctt 3540  
 ccaagccaag taccagatcc gctaccgct ggaggacagc gtggactgga aggtgcccgt 3600  
 cccgccccgg acccgccct gaccccgccc cccgcactctg actcctccct caccgtgcag 3660  
 gtggtggatg acgtcagcaa ccagacctcc tgccgtctcg cgggcctgaa gcccggcacc 3720  
 gtttacttcg tccaagtgcg ttgtaacca ttcgggatct atgggtcgaa aaaggcggga 3780  
 atctggagcg agtggagcca cccaccgct gcctccacc ctcgaagtgg tgagcacctc 3840  
 tccagggtg gctggcccat ggaatccca atccatctg ttccttcccc cccaccctt 3900  
 ttttgagaca gcgtcttcag gtagcgcatg ctggccttaa attcagtatg tagtcaagga 3960  
 tgacctcgag ctctggtct ttttgtctcc acttagagac aatggccagt ggccatcacc 4020  
 accttggga gactagccat ggagtctatt tagcctgtca tttggtgaca gatggagtac 4080  
 aacagtgtga cctcttgtaa gagaactgaa gacaggctgt ttttaacccc aatatacctag 4140  
 gctctctaga ggttaacttt atataaaata gagactatta cagccagtta tcacatggtc 4200  
 ccacagaacc ttttgtcaca caacctatag accacagtgc ctgtgcctac cacataaggg 4260  
 tctctactgc tggcccacc ctccaaccct taaaaggtaa cctaggcagc cttaatattt 4320  
 gcaatcctcc tacctcagcc tcttgaatgc tcagaaacca ggcattaacc caagtttctc 4380  
 ttctctgggt ccttttctta aggtgggagg gcctaaagat gacttcttt gtcctgaaga 4440  
 ctctccgagc ccatggatct gcactctcta atatgaaata tattgcataa aatgtctggc 4500  
 ctcagtttcc ccacctgtca ggtttaggca gcacagtcgg tccaagacac ttcattattt 4560  
 gcaggcagta taagaagaag ctcccatccc ccaccgctt cctccggtcc ctaagacaga 4620

atacttctac actgaaactg aactctcgca gacgcatatg ctcactttaa tgatgatgaa 4680  
 ataatgggga aactgaggct ccgagagatt cctggaggaa gaggggtcaaa accagctcca 4740  
 ggaagctctc cagcccccat ccgggcctct ccaggttctg ggcttggcgg gagtgaacac 4800  
 agctgggagg ggctggagcc tgggagcttt ggcccttgct cgtgcccagc acctgcgatt 4860  
 cttgcacggg agccagcagg cggctgcgtc cgcccgagag actgaagaag ccgggggtag 4920  
 gggttgaggg aggtaagcag gggctgtggg ggccgaagct tgtgccaggg cctgtcagcg 4980  
 agtccccagt tttatttatg gcgtgaggcc gatgtcctta tccgctggcc tgctggggga 5040  
 tggctgcggc tggggattgg acccaagggc tggcttccca ctcagtcctc cagcccactc 5100  
 catgtcacac ccgtgcattc tctgaggctt atcttgggaa cccgcccttg ttctgtgctg 5160  
 tctgtctcta tttctgtcat tcactttccc agagcctttt ttttatgctt ttaataaac 5220  
 tacgttttaa aaattgcttt tgtataatgt gtgtgccttc gtgagcgtgc gtgccacaac 5280  
 acacacgtga aggttagaga actttgttga gtaggctcct tccaccatgt gggactaggg 5340  
 ctggcgacaa gagcaattac tgagtcactc cgccagcccc tcaccctca cttcccatcc 5400  
 tgtttgata gtcataagta atcgaaggta aatcgtggc ttaatttcg tagctatcct 5460  
 gcctcagcct accaagtgt gtgtaccac gtttgtggga ggggctctcc tccagtgctc 5520  
 tgggggtgac acagtcccaa gatctctgct ttctaggtct ttgtcttagt ttgcccttg 5580  
 ctttgtccgt gtccctagag tctccggccc cacttatcca ttgactggtc tttcctttac 5640  
 cgaataactc gttttacctc ccactgattt gactccctcc tttgcttgct tccatcgccg 5700  
 tggcattgcc attcctctgg gtgactctgg gtccacacct gacaccttc ccaactttcc 5760  
 ccagccgaag ctggtctggt atgggaggcc gccgtccgc gcgcgcctcc tgctggccgc 5820  
 gccccaacac tgccgctcca ttctctttag agcgccggg cccgggcggc ggggtgtgcg 5880  
 agccgcgggg cggcgagccc agctcgggcc cgggtgcggc cgagctcaag cagttcctcg 5940  
 gctggctcaa gaagcacgca tactgctcga accttagttt ccgcctgtac gaccagtggc 6000  
 gtgcttgat gcagaagtca cacaagacct gaaaccaggt aggaaagttg ggggaggctt 6060  
 gcgtgggggg taaaggagca gaggaagaga gagaccggg tgagcagcct ccacaacacc 6120  
 gcactcttct ttccaagcac aggacgaggg gatcctgccc tcgggcagac ggggtgcggc 6180  
 gagaggtaag ggggtctggg tgagtggggc ctacagcagt ctatagagg ccctttcccc 6240  
 tccttcggtg ttgctcaaag ggatctctta gtgctcattt caccactgc aaagagcccc 6300  
 aggttttact gcatcatcaa gttgctgaag ggtccaggct taatgtggcc tcttttctgc 6360

cctcaggtcc tgccggctaa actctaagga taggcatcc tcctgctggg tcagacctgg 6420  
aggctcacct gaattggagc ccctctgtac catctgggca acaaagaaac ctaccagagg 6480  
ctgggcacaa tgagctccca caaccacagc tttgggtccac atgatgggtca cacttgata 6540  
taccacagtg tgggtagggg tggggtattg cagggcctcc caagagtctc tttaaataaa 6600  
taaaggagtt gttcaggtcc cgatggccag tgtgtttggg gcctatgtgc tggggtgggg 6660  
gga 6663

<210> 29  
<211> 186  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown Organism: Murine NR6

<220>  
<221> UNSURE  
<222> (136)  
<223> Unsure at position 136

<220>  
<221> UNSURE  
<222> (139)  
<223> Unsure at positionn 139

<220>  
<221> UNSURE  
<222> (162)  
<223> Unsure at position 162

<220>  
<221> UNSURE  
<222> (177)  
<223> Unsure at position 177

<400> 29  
Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser Ile  
1 5 10 15  
His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr Phe  
20 25 30  
Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr Ser  
35 40 45  
Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln Ser  
50 55 60  
Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala Gly  
65 70 75 80



Leu Leu Met Leu Phe His Leu Gly Leu Gln Ala Ser Ile Ser  
                   20                                  25                                  30

<210> 33  
 <211> 23  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:3' UTR

<400> 33  
 Ile Lys Pro Ser Gly Arg Arg Gly Ala Ala Arg Gly Pro Ala Gly Asp  
   1                                  5                                  10                                  15

Tyr Lys Asp Asp Asp Asp Lys  
                   20

<210> 34  
 <211> 73  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:3' UTR

<400> 34  
 gatcttgccc tcgggcagac ggggtgcggc gagaggtcct gccggcgact acaaggacga 60  
 cgatgacaag tag 73

<210> 35  
 <211> 73  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:3' UTR

<400> 35  
 aacgggagcc cgtctgcccc acgccgctct ccaggacggc cgctgatgtt cctgctgcta 60  
 ctgttcaccc tag 73

<210> 36  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Oligonucleotide  
                   2199

<400> 36  
cccacgcttc tcatcggatt ctccctg 27

<210> 37  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Oligonucleotide  
2200

<400> 37  
cagtccacac tgcctccac tcggtag 27

<210> 38  
<211> 11832  
<212> DNA  
<213> Unknown

<220>  
<223> Description of Unknown Organism:Murine NR6 gene

<400> 38  
gcggccgctg cagtgattac tcaccgctg gcgcacccca cccgcggggc gctgagtgga 60  
tttttccgtg gggggatgtg aagaagtta gggagaactc ttctgcaccg atgggaacta 120  
ggaatgcagg gttcgggtccc gttccccaaa ggacacacct ctcccataa gccactcat 180  
aagggtctccc tgcacgctc cggggacatc cccatatcca ataccgcag atatgatagt 240  
tgagaaggga ccagaggccg gagactccct cctgccttc tggctttccc cccccctgc 300  
acgaaacgag actacagcga tgggagaggt ggcataagc cttagggtgg ggatcggtag 360  
gacccatgca cccagagaaa gggactggtg gcaactttca aactctctgg ggaaggaaga 420  
agggctgaaa gaggatgaac gggctcaggt actgctcaat gtgtgtgtgg cggaccaaag 480  
tgggtatggg ggccccgtaa gaggggaggg gaaggtggat aggaaggatc ccggtagact 540  
ggaggggatc ctggaaaagc accagggctg cgagctagga accattcgg agttaagggt 600  
acaggatccc agatgagggg gtgggaagcc tgggacgggc gggaccagag agggaggtcc 660  
cacgggctgg tggggaaaga gtggggggct tcgcgcagga ggatgggacg ttcaggagtg 720  
gtaactgggc ggaggccggc cgggcggggc gcgcggtgcc cgcgggcggg ggaaggccg 780  
gtgcggggcc cacgatcaac cccccccag gggccggggc gggccggggg cggggccggg 840  
cggggcgagc ggcgcattag cgccttgtca atttcggctg ctccagactg ctccggcctt 900  
cgctgtccgc gccagtgac gcgcgtgagg acccgagccc caatctgcac cccgcagact 960

cgcccccgcc ccataccggc gttgcagtca ccgcccgttg cgcgccaccc ccatgccccg 1020  
 gggtcgcccc ggccccgtcg cccaatccgc gcggcgcccg ccgcggccgc tgtcctcgct 1080  
 gtggtcgcct ctgttgctct gtgtcctcgg ggtgcctcgg ggcggatcgg gagccccgtga 1140  
 gtaccgtgcg ccctgctccc cacctcccca gggaagccgg gatccggcgc cccgggggggt 1200  
 agtcgcgggg gatggaagaa ggggcgcgag cgccacctgg acgtcccggg aacaaaggaa 1260  
 ggcgggccctc ggggcgcctt cacctgtggg gctcatggca ccaccacca gcctcccaag 1320  
 agtaccctgt tatacatcag aggcctctta tctgtatccc ctttgcgagg ctgtctggcc 1380  
 aggctcagtt tgaaggacat cgcagtgtcc tgggaccccc ctcttcagg gtgctgggac 1440  
 gcttcggggc gcacgcctgt gtcttgata tcagagcgga agggaagcct ccctggcccg 1500  
 gggcgcacgc ttgggtgcgt tgggttgggt gctggcgcaa agtgggggtcc cctcccccat 1560  
 gaagtgatga tccccggggg gaggggtgggg cgttatcgtg agccctcctg tccgcctggc 1620  
 atgcggcccc gcgtccctcg ggacttgctt ctccgtgggg tcggcgccgc cccctcccc 1680  
 ctatagcaga ctccatgctt tggatatctc gaagtcctct cactgggtgg ggctcacaac 1740  
 cggctctatt caggctgcgc tgggttgaga gcctctagcg actgaaattt cggtgaggag 1800  
 cgagagcaag cgtgtccggg caccgcgagc ccagacttca ttgtctaagg ggcacccagt 1860  
 ggggggtcagc tgccgagaga atcccactgt ccaggagga actcctggcc ttgagcccc 1920  
 atcacccaac gcacacatcc ccgccaggat gcggtctcca catccagacc ctctctggga 1980  
 cacacccaaa gacacacaaa agagccccac tggcttatgt cccgtcacc tgccctccga 2040  
 cgcgcgctgc agcccagatg cgtattcgca caccatcgcg gcgctcgcat tccatcctct 2100  
 acacacacac acacacacac acacacacac acacacacac acacacagac acgcacacac 2160  
 acacgcacgc acacacacgc acgcccgcac tcgtgggtccc acatttattt cacaggggag 2220  
 gcaacaccgg ggtacgcata tgggtgagt cactggagat ctttccccac cactctcagg 2280  
 acccatccg gagacacagg ccacaccgca ggggcaccac gctgcgctgc tgctctgggc 2340  
 tagtagtctt gtgcagtttg tccgcggtgt ctgtggacgc cctcccgtc ttgtcagggg 2400  
 acaggaacct aactcctgc ttgcccaagg cggctgggca ggtgatgtgg tgacaccgg 2460  
 gacctttccg gggagttggg gttgctgcc agcctgggta gtttttgaat gccaccaata 2520  
 gcgctaagct ttgtttccgg gcgggctgca gagcaacagg cgaaggtggc ggagtggggg 2580  
 tggcgcgctgt gttttttctt ttaaggggga gagaaattaa ataagagggt ctcacacctc 2640  
 tgcaatctgt ttgtacttac cgtgtgtctt aacacctgac cagccagccg gtgggtcgta 2700



aaagtgtatg caggtaccag cgggacagga gatgggggcc cctgggggtat ggctgggatg 2760  
gaggccacct tcccgttggc ctttcagga atctcacact tttccctttt aaaacacatg 2820  
gtgttctttt taataacggc agcaactccg cattgggaaa gggggaaata agcttgtata 2880  
ggccccggct ttgtggaaag gaggggaaga gggaagaaaa aaggaggggt gtctcctcca 2940  
ggcttagggg gctgtcagct gctgctctgt ctagcttggc atgtgtgtgc cccagtcccc 3000  
agtggctttg gccattgtt tgtggaagcc aagagggaga ctggagtcct ctatctctgg 3060  
tactccagag tcaggcttct cagtccgagc ccagagaacg tcttcctgt tttatggagg 3120  
gaatcagga aggggtgcc aggtggacta cgttctgctg aggactgtac cagtcgctcg 3180  
aaggagaaag cttgggcttg cccccctcc cctcaagcc acgaaggga gctgctaggc 3240  
tagtgtgta aaagggcatt actcccagc caggacccc cagagagtcc ccttcctggc 3300  
cagacaaatg ctggggaggg acagaggggt gtgatcattg cccaggagtg cagacagtgg 3360  
ggtcccgggt cgggcagtgc ctcccacct gctgaggggg gcgcccaggc aggaagcggg 3420  
gggtgggccg gggtagagac gctggcacgt cccagttcat gccgaaggaa ttctgaatta 3480  
gcgggcggct ggctgcctgg gacctccggg gcggccccct ggcccccgcc gctccgtctg 3540  
gcctgtcct cctgtcctt cgcacggacg ctgagacctc cgctgagccc tgggacaagc 3600  
cccaaatgca actgcgattg caggcttcgc aagaccgcc tcctcccaag gccaaatttg 3660  
cctgggagaa gtcattcagg gccagacta gaaccatgtt ggtgccacct catccatctg 3720  
gggcatgaag gaccgtccag ggctgcagtt tagcttctta ataggaacct gggggtgggt 3780  
gcagcctctg ttctccgagc ctctttggaa atcggttttg tttttgtttt tgttttttcc 3840  
aatactcttt tcctctcatc ccatccggg actgttttcc tcctaagggt ttgagagccc 3900  
tgcagtcttc cctaaccttt tctttgcttc taccaggg cctttgcaca tggagtccca 3960  
cctctccct tgcccaactg gggctccagc cttactgcat ttggctcttg gtaactgtcc 4020  
cagggcctct ctgacacaca gggttgtagc cccagctccc tctcttctcc tcccccttt 4080  
ctcttttgct tctgagactt aattttttct tttttctttt tggctttttg agacagggtt 4140  
tctctgtaca gccctggctg ccctggcact cattctgtag accaggctag cctcaaactc 4200  
acaaacctac ctgcctctgc ctttccagt ctggcactaa agatgtgggc caccacaact 4260  
agtagttaag tgttttgctg tgtctttatt cctatagtga cctcagttcc tggcatattg 4320  
taggcgatgg atggatgaat ggatggatgg atggatggat ggatggttgg atggagcaag 4380  
cttgaatcgt cctgagtga aaaagagacc tcagagaact gaatggagt aggttcccag 4440

ggcagcctgg cctgctggtc tcatgggagc tccctgtgaa acttccccca cacctcccac 4500  
 caccctgccca tccctgtgtgg ctgacaagaa aggccaatgg ccagatgggg acacagactc 4560  
 agggaaagctt ggaatatgtt cccctcctca taccctaggc cttgttgtcc ccctgagggc 4620  
 ccagcctatg agtagggcag ctgtgggctg ccctaagggt gggtaggcaa gaaggggggtg 4680  
 gtccctcagg gtgggtcaca ggattgaggt catttccaaa gtggccatca cagtggccct 4740  
 aggaaatgat tgtggagagt cagaactcct gttgggaggt gtagagggcc ttgcatgtgg 4800  
 gcttctgtgg ctgtcccttc tcttgtggtc ctttgcacag tcccctcgtg tgtgctggga 4860  
 tgtgaggagg gcacggggaa aatgaaggct cagccctca gcttgccctt cacggttcac 4920  
 ccaacagggc tcacctctcc tctggacagg ctctcactgt atgcacagat tggcctcaca 4980  
 tttgattccc ttcctttggg ctccctggat gacaaacatt taccagggtg ggattttaca 5040  
 ttttagatat gtccattctc cagaaacaca cttgtgaggt tagggatatca gtgaaaggac 5100  
 accaccagga cagacaaaga attggagagg aaggaaattg gtaagccagg ccatgcttga 5160  
 tggcttatgt gtaatcccag aactctggac gctgaggcag gaggattcca agtttcaaga 5220  
 cagtgtgttc taggtaatga gaccctgtca agaaaagaaa agaaataaag agacaagaaa 5280  
 atgtttatag gctgtgagac agcttgggtg gtaaggggca cttgcctcca atcaagatga 5340  
 cctcagcccc atccctagga atccatggta gaaggagaaa gcaaactcca gctgctgacc 5400  
 tccatacatg tgcaccaatg tgcacacaca caggagagaca taatcaatta ataggatgta 5460  
 tttgcttaga tttgagtagg catttatgac tgatgtttta aaatttttat ttgattttat 5520  
 gaaaatatac ctgtttgtat ttggtttggg ttggtttgag ttttgtttat ttgagacagg 5580  
 gcttctctgt gtagtcctgg ctgtccttgg aactcactct gtagaccagg ctggccttga 5640  
 actcagaaat ccgcctgctt gtgcttccca agtgcttaga ttaaagggtg gcactgccat 5700  
 tcagcaaaat tgcatacttt aaccccagta tttgggaggc agaggcagac taatgtgtga 5760  
 attccaggct agccaaggat acagagttag accctattct taccctcccc ccccaaaacc 5820  
 ccaaaatgta ttttgtgctt gtgtatgtac atgtgtgttg cagcacgtaa atgtccaagg 5880  
 acaacttgta gaagttctct ccgttcacag tctaagtcct gaattcaaac taaggtcctc 5940  
 aggcttagcc acagtcttct ttatgtactg agccatttca ctggccctgg attgactgat 6000  
 gaattaattt ttgagataag gtctcttgta gctctagcta ggctcaaact atgaactccc 6060  
 aaggctcatct tgagctgctg gtactcttgc ttccaccca agtggtggaa tgatactcag 6120  
 gcagcacttc tctggggaag gggctggcct tggccttgat tttgttgcct cagcttcaat 6180

gagtgccttgg gtctcgttgt ttcttttctt tatctgtgaa atgggtgaac acctgttcaa 6240  
gacttcctga ctcttgaaac atccaggcag ggtgaggac ttgaagtggg ctcatcccat 6300  
gcctaacaaa gtgtcgtctt tgaccccaga cacagctgta atcagcccc aggacccac 6360  
ccttctcatc ggctcctccc tgcaagctac ctgctctata catggagaca cacctggggc 6420  
caccgctgag gggctctact ggaccttcaa tggctgccgc ctgccctctg agctgtcccg 6480  
cctccttaac acctccacce tggccctggc cctggctaac cttaatgggt ccaggcagca 6540  
gtcaggagac aatctggtgt gtcacgccgc agacggcagc attctggctg gctcctgcct 6600  
ctatgttggc tgtaagtggg gccccagaca ctacagagata gatgggggtt ggcaatgaca 6660  
gatttagagc ctgggtcttc tgtcctgggg cagagccatg ggctctcact tgcattgcagg 6720  
catggtcata ccagcacag gcattgcaac tctagggaca gctgtggctg cactgtcccc 6780  
tgtgtacccc acagctttag aaaagctgtc atgttttctt tgtagtggc cctgagaagc 6840  
cctttaacat cagctgctgg tcccgggaaca tgaaggatct cacgtgccgc tggacaccgg 6900  
gtgcacacgg ggagacattc ttacatacca actactccct caagtacaag ctgaggttgg 6960  
taccagcca agccttgctg tgtgacttct ggcaatactt accttctctg atcaaatatg 7020  
ttcctgttta tgaactcaaa agggactctc gcacctccac aggtggtacg gtcaggataa 7080  
cacatgtgag gagtaccaca ctgtggggcc tactcatgc catatcccca aggacctggc 7140  
cctcttctact ccctatgaga tctgggtgga agccaccaat cgcctaggct cagcaagatc 7200  
tgatgtcctc aactggatg tcctggacgt gggtagagccc ccagtgtcca cctgtgttct 7260  
gccctagacc ttatagggcg cctccccccc atccccccag acttttttgt tcttctagag 7320  
gtcttagcca cagccacggt ggttgcagga cagtgggtgt tcataactta atgcaaagac 7380  
tttccccaa gacagtcaag attttccct cccaccccc aacacacaca tacacacaca 7440  
ctctgcagag aacacctggc ctgaccacce tccctctcta cagcccagggt gttcagaagg 7500  
gagtcctagg ggactgagag gaggcgcca ggtctgaagg cgcgccagga agccgaggcc 7560  
ttgagctggg gggggggggc aggggttgag gcacgaactg gatgatccct gagcacaact 7620  
gggcctaata taattagggt gttcccagcc caaagcagcc tgggccattt aaccttcaa 7680  
gtgcctcact gaagactcag gggagagatc agcttgact ctctccatgg tccccagga 7740  
gggttctctg gtgcccctgg ctcatccca catccagagg ttttgtgtct tcctggcatc 7800  
taacctcag ttgtgctctg tggctggcac agctgcccc tggaggctct tggtaatgta 7860  
caaggcatca gaggtggaca tgggatggg atacataggg atggagccaa atagcacctc 7920

aaggtgggggt gatatacaat aaagcttgct accctgacgc tcagaaagcc tactcatgat 7980  
gatcacaatt gttgacatca ctctgggaca tgtagtgaga ccctagctca aaacacagac 8040  
agtagcttta agagtcagct tgtgacttaa tactggaact cagggcctaa taggtgctgg 8100  
gtgatgctcg cctcactccc tgtttagtga gatctctgcg ctaatctcca cccagctgg 8160  
gtgggctgct ctgtcccctt gagggcagga atgtgtgtct tccatcagag ataggacccg 8220  
tggtagcagc aactgctgct ggctgtttct ggaatattaa atgacagtaa tctatcaggc 8280  
ctgggtgagt agctaacagg ggtgggggcg tggctctgga aacgcagata gggcatagg 8340  
agccactgca gcctagatta caccactggg tgttctgtca ctaggccatt ctcaccaagc 8400  
agtcctcaga actgggagca ctgttgccag catttaatgc cagcatttaa tgccagcatt 8460  
aggggaggca gaggcagaag gatctctctg agttcaaggc catcctgaat ttacataaag 8520  
agctccaggc cagccagggt gcgcagtaaa acctgtctc aaaaaacaaa gcatctttag 8580  
tgaccaggct tgctccaccc ccagtgacca cggaccccc acccgacgtg cacgtgagcc 8640  
gcgttggggg cctggaggac cagctgagtg tgcgctgggt ctcaccacca gctctcaagg 8700  
atttcctctt ccaagccaag taccagatcc gctaccgct ggaggacagc gtggactgga 8760  
aggtgcccggt cccgccccgg acccgcccct gaccccgccc cccgcatctg actcctccct 8820  
caccgtgcag gtggtggatg acgtcagcaa ccagacctcc tgccgtctcg cgggcctgaa 8880  
gcccggcacc gtttacttcg tccaagtgcg ttgtaacca ttcgggatct atgggtcgaa 8940  
aaaggcggga atctggagcg agtgaggcca cccaccgct gcctccaccc ctcgaagtgg 9000  
tgagcacctc tccagggtg gctggcccat ggaatcccca atccatcctg ttccttcccc 9060  
cccacccttt ttttgagaca gcgtcttcag gtagcgcag ctggccttaa attcagtatg 9120  
tagtcaagga tgacctcgag ctctgggtct ttttgtctcc acttagagac aatggccagt 9180  
ggccatcacc acctttggga gactagccat ggagtctatt tagcctgtca tttggtgaca 9240  
gatggagtac aacagtgtga cctcttgtaa gagaactgaa gacaggctgt ttttaacccc 9300  
aatatcctag gctctctaga ggttaacttt atataaaata gagactatta cagccagtta 9360  
tcacatggtc ccacagaacc ttttgtcaca caacctatag accacagtgc ctgtgcctac 9420  
cacataaggg tctctactgc tggcccaccc ctccaacct taaaaggtaa cctaggcagc 9480  
cttaatattht gcaatcctcc tacctcagcc tcttgaatgc tcagaaacca ggcattaacc 9540  
caagtttctc ttctctgggt ccctttctta aggtgggagg gcctaaagat gacttccttt 9600  
gtcctgaaga ctctccgagc ccatggatct gcactctcta atatgaaata tattgcataa 9660

aatgtctggc ctcagtttcc ccacctgtca ggtttaggca gcacagtcgg tccaagacac 9720  
ttcattatth gcaggcagta taagaagaag ctcccatccc ccacccgctt cctccgggtcc 9780  
ctaagacaga atactttctac actgaaactg aactctcgca gacgcatatg ctcactttta 9840  
tgatgatgaa ataatgggga aactgaggct ccgagagatt cctggaggaa gaggggtcaaa 9900  
accagctcca ggaagctctc cagcccccat ccgggcctct ccaggttctg ggcttggcgg 9960  
gagtgaacac agctgggagg ggctggagcc tgggagcttt ggcccttgct cgtgcccagc 10020  
acctgcgatt cttgcacggg agccagcagg cggctgcgtc cgcccgagag actgaagaag 10080  
ccgggggtag gggttgaggg aggtaagcag gggctgtggg ggccgaagct tgtgccaggg 10140  
cctgtcagcg agtccccagt tttatthtatg gcgtgaggcc gatgtcctta tccgctggcc 10200  
tgctggggga tggctgcggc tggggattgg acccaagggc tggcttccca ctcagtcctc 10260  
cagcccactc catgtcacac ccgtgcattc tctgaggctt atcttgaggaa cccgcccttg 10320  
ttctgtgctg tctgtctcta tttctgtcat tcactttccc agagcctttt ttttatgctt 10380  
ttaatataac tacgttttaa aaattgcttt tgtataatgt gtgtgccttc gtgagcgtgc 10440  
gtgccacaac acacacgtga aggttagaga actttgttga gtaggtcct tccaccatgt 10500  
gggactaggg ctggcgacaa gagcaattac tgagtcattc cgccagcccc tcaccctca 10560  
cttcccatcc tgtttggata gtcataaggta atcgaaggta aatcgctggc ttaatttcg 10620  
tagctatcct gcctcagcct accaagtgtc gtgtaccac gtttgtggga ggggctctcc 10680  
tcccagtgtc tgggggtaca cagtcccaag atctctgctt tctaggtctt tgtcttagtt 10740  
tgcccttgcc tttgtccgtg tccctagagt ctccggcccc acttagtctc cattgatttc 10800  
ctttctgacc gaatactcg ttttacctcc cactgatttg actccctcct ttgcttgtct 10860  
ccatcgccgt ggcattgcca ttctcttggg tgactctggg tccacacctg acacctttcc 10920  
caactttccc cagccgaagc tggctctggta tgggaggccg ccgtcccggc cgcgcctcct 10980  
gctggccggc ccccaacact gccgctccat tctctttaga gcgccggggc ccgggaggcg 11040  
gggtgtgcca gccgcggggc ggcgagccca gctcggggcc ggtgcgggcg gagctcaagc 11100  
agttcctcgg ctggctcaag aagcacgcat actgctcgaa ccttagtttc cgcctgtacg 11160  
accagtggcg tgcttgatg cagaagtcac acaagaccgg aaaccaggta ggaaagtgg 11220  
gggaggcttg cgtgggggggt aaaggagcag aggaagagag agaccgggt gagcagctc 11280  
cacaacaccg cactcttctt tccaagcaca ggacgagggg atcctgccct cgggcagacg 11340  
gggtgcggcg agaggtaagg gggctctgggt gagtggggcc tacagcagtc tagatgaggc 11400

cctttccctt ccttcggtgt tgctcaaagg gatctcttag tgctcatttc acccactgca 11460  
 aagagcccca ggttttactg catcatcaag ttgctgaagg gtccaggctt aatgtggcct 11520  
 cttttctgcc ctcaggctct gccggctaaa ctctaaggat aggccatcct cctgctgggt 11580  
 cagacctgga ggctcacctg aattggagcc cctctgtacc atctgggcaa caaagaaacc 11640  
 taccagaggc tgggcacaat gagctccac aaccacagct ttggtccaca tgatggtcac 11700  
 acttgatat accccagtgt gggtaggggt ggggtattgc agggcctccc aagagtctct 11760  
 ttaaataaat aaaggagttg ttcaggctcc gatggccagt gtgtttgggg cctatgtgct 11820  
 ggggtggggg ga 11832

<210> 39  
 <211> 26  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Murine peptide

<400> 39  
 Val Ile Ser Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln  
 1 5 10 15  
 Ala Thr Cys Ser Ile His Gly Asp Thr Pro  
 20 25

<210> 40  
 <211> 21  
 <212> DNA  
 <213> Oligonucleotide Sequence

<400> 40  
 gtccaagtgc gttgtaaccc a 21

<210> 41  
 <211> 24  
 <212> DNA  
 <213> Oligonucleotide Sequence

<400> 41  
 gctgagtgtg cgctgggtct cacc 24

<210> 42  
 <211> 18  
 <212> DNA  
 <213> Oligonucleotide Sequence

<400> 42  
ggctccactc gctccaga

18

<210> 43  
<211> 2079  
<212> DNA  
<213> Unknown

<220>  
<221> CDS  
<222> (513)..(1775)

<220>  
<223> Description of Unknown Organism: Nucleotide Sequence of NR6

<400> 43  
gcggtatttg tgtttcaaat ctatctacag aaaagattga gaaccagaag cccttttcgt 60  
  
tttttgaaag ctagctgact cactgttcaa gaaaggagaa cactttcaat tatgctgttt 120  
  
gactgcagtg tcagggatcc aaaggaaatg actccatccc ttccctttca tcccaacctc 180  
  
agtgcacagca aattctgatg tgactgaggg ttggcttggtg aaggagtcac taggaaattc 240  
  
tgcctaagcc atagcgcgat gagaaggatg taccctatgg tgggtatttt cctgtgcccc 300  
  
ctcagaggaa agttgtcaga tgagcagggtg gagtattcta tagcaaacag caagctaata 360  
  
ggttacacag ataactctct gactttgcct tacagaacct gtgctattga ccttagggca 420  
  
aggttcatgc tcagggggcc aactctgtgg gttaggattt gagtttaagc agcttctgct 480  
  
catatttcag cgcccccgcc agcgccggcc cc atg ccc gcc gcc cgc cgg gcc 533  
Met Pro Ala Gly Arg Arg Gly  
1 5  
  
ccc gcc gcc caa tcc gcg cgg cgg ccg ccg ccg ttg ctg ccc ctg ctg 581  
Pro Ala Ala Gln Ser Ala Arg Arg Pro Pro Pro Leu Leu Pro Leu Leu  
10 15 20  
  
ctg ctc tgc gtc ctc ggg gcg ccg cga gcc gga tca gga gcc cac aca 629  
Leu Leu Cys Val Leu Gly Ala Pro Arg Ala Gly Ser Gly Ala His Thr  
25 30 35

gct gtg atc agt ccc cag gat ccc acg ctt ctc atc ggc tcc tcc ctg	677
Ala Val Ile Ser Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu	
40 45 50 55	
ctg gcc acc tgc tca gtg cac gga gac cca cca gga gcc acc gcc gag	725
Leu Ala Thr Cys Ser Val His Gly Asp Pro Pro Gly Ala Thr Ala Glu	
60 65 70	
ggc ctc tac tgg acc ctc aat ggg cgc cgc ctg ccc cct gag ctc tcc	773
Gly Leu Tyr Trp Thr Leu Asn Gly Arg Arg Leu Pro Pro Glu Leu Ser	
75 80 85	
cgt gta ctc aac gcc tcc acc ttg gct ctg gcc ctg gcc aac ctc aat	821
Arg Val Leu Asn Ala Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn	
90 95 100	
ggg tcc agg cag cgg tgc ggg gac aac ctc gtg tgc cac gcc cgt gac	869
Gly Ser Arg Gln Arg Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp	
105 110 115	
ggc agc atc ctg gct ggc tcc tgc ctc tat gtt ggc ctg ccc cca gag	917
Gly Ser Ile Leu Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu	
120 125 130 135	
aaa ccc gtc aac atc agc tgc tgg tcc aag aac atg aag gac ttg acc	965
Lys Pro Val Asn Ile Ser Cys Trp Ser Lys Asn Met Lys Asp Leu Thr	
140 145 150	
tgc cgc tgg acg cca ggg gcc cac ggg gag acc ttc ctc cac acc aac	1013
Cys Arg Trp Thr Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn	
155 160 165	
tac tcc ctc aag tac aag ctt agg tgg tat ggc cag gac aac aca tgt	1061
Tyr Ser Leu Lys Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys	
170 175 180	
gag gag tac cac aca gtg ggg ccc cac tcc tgc cac atc ccc aag gac	1109
Glu Glu Tyr His Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp	
185 190 195	
ctg gct ctc ttt acg ccc tat gag atc tgg gtg gag gcc acc aac cgc	1157
Leu Ala Leu Phe Thr Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg	
200 205 210 215	
ctg ggc tct gcc cgc tcc gat gta ctc acg ctg gat atc ctg gat gtg	1205



Leu	Gly	Ser	Ala	Arg 220	Ser	Asp	Val	Leu	Thr 225	Leu	Asp	Ile	Leu	Asp 230	Val		
gtg	acc	acg	gac	ccc	ccg	ccc	gac	gtg	cac	gtg	agc	cgc	gtc	ggg	ggc	1253	
Val	Thr	Thr	Asp 235	Pro	Pro	Pro	Asp	Val 240	His	Val	Ser	Arg	Val 245	Gly	Gly		
ctg	gag	gac	cag	ctg	agc	gtg	cgc	tgg	gtg	tcg	cca	ccc	gcc	ctc	aag	1301	
Leu	Glu	Asp 250	Gln	Leu	Ser	Val	Arg 255	Trp	Val	Ser	Pro	Pro	Ala	Leu	Lys		
gat	ttc	ctc	ttt	caa	gcc	aaa	tac	cag	atc	cgc	tac	cga	gtg	gag	gac	1349	
Asp	Phe 265	Leu	Phe	Gln	Ala	Lys 270	Tyr	Gln	Ile	Arg	Tyr 275	Arg	Val	Glu	Asp		
agt	gtg	gac	tgg	aag	gtg	gtg	gac	gat	gtg	agc	aac	cag	acc	tcc	tgc	1397	
Ser 280	Val	Asp	Trp	Lys	Val 285	Val	Asp	Asp	Val	Ser 290	Asn	Gln	Thr	Ser	Cys 295		
cgc	ctg	gcc	ggc	ctg	aaa	ccc	ggc	acc	gtg	tac	ttc	gtg	caa	gtg	cgc	1445	
Arg	Leu	Ala	Gly	Leu 300	Lys	Pro	Gly	Thr	Val 305	Tyr	Phe	Val	Gln	Val 310	Arg		
tgc	aac	ccc	ttt	ggc	atc	tat	ggc	tcc	aag	aaa	gcc	ggg	atc	tgg	agt	1493	
Cys	Asn	Pro	Phe 315	Gly	Ile	Tyr	Gly	Ser 320	Lys	Lys	Ala	Gly	Ile 325	Trp	Ser		
gag	tgg	agc	cac	ccc	aca	gcc	gcc	tcc	act	ccc	cgc	agt	gag	cgc	ccg	1541	
Glu	Trp	Ser 330	His	Pro	Thr	Ala	Ala 335	Ser	Thr	Pro	Arg	Ser 340	Glu	Arg	Pro		
ggc	ccg	ggc	ggc	ggg	gcg	tgc	gaa	ccg	cgg	ggc	gga	gag	ccg	agc	tcg	1589	
Gly	Pro 345	Gly	Gly	Gly	Ala	Cys 350	Glu	Pro	Arg	Gly	Gly 355	Glu	Pro	Ser	Ser		
ggg	ccg	gtg	cgg	cgc	gag	ctc	aag	cag	ttc	ctg	ggc	tgg	ctc	aag	aag	1637	
Gly 360	Pro	Val	Arg	Arg	Glu 365	Leu	Lys	Gln	Phe	Leu 370	Gly	Trp	Leu	Lys	Lys 375		
cac	gcg	tac	tgc	tcc	aac	ctc	agc	ttc	cgc	ctc	tac	gac	cag	tgg	cga	1685	
His	Ala	Tyr	Cys	Ser 380	Asn	Leu	Ser	Phe	Arg 385	Leu	Tyr	Asp	Gln	Trp 390	Arg		
gcc	tgg	atg	cag	aag	tcg	cac	aag	acc	cgc	aac	cag	gac	gag	ggg	atc	1733	
Ala	Trp	Met	Gln 395	Lys	Ser	His	Lys	Thr 400	Arg	Asn	Gln	Asp	Glu 405	Gly	Ile		

ctg ccc tcg ggc aga cgg ggc acg gcg aga ggt cct gcc aga 1775  
 Leu Pro Ser Gly Arg Arg Gly Thr Ala Arg Gly Pro Ala Arg  
           410                          415                          420  
 taagctgtag gggctcaggc caccctccct gccacgtgga gacgcagagg ccgaacccaa 1835  
 actggggcca cctctgtacc ctcacttcag ggcacctgag ccaccctcag caggagctgg 1895  
 ggtggcccct gagctccaac ggccataaca gctctgactc ccacgtgagg ccacctttgg 1955  
 gtgcacccca gtgggtgtgt gtgtgtgtgt gagggttggt tgagttgcct agaaccctg 2015  
 ccagggctgg gggtgagaag gggagtcatt actccccatt acctagggcc cctccaaaag 2075  
 atcc 2079

<210> 44  
 <211> 421  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Description of Unknown Organism: Amino Acid Sequence of NR6

<400> 44  
 Met Pro Ala Gly Arg Arg Gly Pro Ala Ala Gln Ser Ala Arg Arg Pro  
   1                          5                          10                          15  
 Pro Pro Leu Leu Pro Leu Leu Leu Leu Cys Val Leu Gly Ala Pro Arg  
           20                          25                          30  
 Ala Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro Gln Asp Pro Thr  
           35                          40                          45  
 Leu Leu Ile Gly Ser Ser Leu Leu Ala Thr Cys Ser Val His Gly Asp  
   50                          55                          60  
 Pro Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr Leu Asn Gly Arg  
   65                          70                          75                          80  
 Arg Leu Pro Pro Glu Leu Ser Arg Val Leu Asn Ala Ser Thr Leu Ala  
           85                          90                          95  
 Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Arg Ser Gly Asp Asn  
           100                          105                          110  
 Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala Gly Ser Cys Leu  
           115                          120                          125  
 Tyr Val Gly Leu Pro Pro Glu Lys Pro Val Asn Ile Ser Cys Trp Ser

130				135				140							
Lys 145	Asn	Met	Lys	Asp	Leu 150	Thr	Cys	Arg	Trp	Thr 155	Pro	Gly	Ala	His	Gly 160
Glu	Thr	Phe	Leu	His 165	Thr	Asn	Tyr	Ser	Leu 170	Lys	Tyr	Lys	Leu	Arg	Trp 175
Tyr	Gly	Gln	Asp 180	Asn	Thr	Cys	Glu	Glu 185	Tyr	His	Thr	Val	Gly 190	Pro	His
Ser	Cys	His 195	Ile	Pro	Lys	Asp	Leu 200	Ala	Leu	Phe	Thr	Pro	Tyr	Glu	Ile
Trp	Val 210	Glu	Ala	Thr	Asn	Arg 215	Leu	Gly	Ser	Ala	Arg	Ser	Asp	Val	Leu
Thr 225	Leu	Asp	Ile	Leu	Asp 230	Val	Val	Thr	Thr	Asp 235	Pro	Pro	Pro	Asp	Val 240
His	Val	Ser	Arg	Val 245	Gly	Gly	Leu	Glu	Asp 250	Gln	Leu	Ser	Val	Arg	Trp 255
Val	Ser	Pro	Pro	Ala 260	Leu	Lys	Asp	Phe 265	Leu	Phe	Gln	Ala	Lys	Tyr	Gln 270
Ile	Arg	Tyr 275	Arg	Val	Glu	Asp	Ser 280	Val	Asp	Trp	Lys	Val	Val	Asp	Asp 285
Val 290	Ser	Asn	Gln	Thr	Ser	Cys 295	Arg	Leu	Ala	Gly	Leu	Lys	Pro	Gly	Thr 300
Val 305	Tyr	Phe	Val	Gln	Val 310	Arg	Cys	Asn	Pro	Phe 315	Gly	Ile	Tyr	Gly	Ser 320
Lys	Lys	Ala	Gly	Ile 325	Trp	Ser	Glu	Trp	Ser 330	His	Pro	Thr	Ala	Ala	Ser 335
Thr	Pro	Arg	Ser 340	Glu	Arg	Pro	Gly	Pro	Gly 345	Gly	Gly	Ala	Cys	Glu	Pro 350
Arg	Gly	Gly 355	Glu	Pro	Ser	Ser	Gly 360	Pro	Val	Arg	Arg	Glu	Leu	Lys	Gln 365
Phe 370	Leu	Gly	Trp	Leu	Lys	Lys 375	His	Ala	Tyr	Cys	Ser	Asn	Leu	Ser	Phe 380
Arg 385	Leu	Tyr	Asp	Gln	Trp 390	Arg	Ala	Trp	Met	Gln 395	Lys	Ser	His	Lys	Thr 400
Arg	Asn	Gln	Asp	Glu 405	Gly	Ile	Leu	Pro	Ser 410	Gly	Arg	Arg	Gly	Thr	Ala 415
Arg	Gly	Pro	Ala	Arg 420											

<210> 45  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<223> Description of Artificial Sequence: Fwd Primer

<400> 45  
tgccccaga gaaaccgtc aac 23

<210> 46  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Rev Primer

<400> 46  
cgtgagtaca tcggagcggg cagag 25

<210> 47  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligonucleotide

<400> 47  
tcaggcgcgc cttgccaca cagctgtgat c 31.

<210> 48  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligonucleotide

<400> 48  
tcaggcgcgc cttatctgg caggacctct 30

<210> 49  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligonucleotide

<400> 49  
tcaggcgcgc ctgcccgcgc gccgc 25

<210> 50  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligonucleotide

<400> 50  
ataaggcgcgc ccctggcagg acctctcg 28

<210> 51  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligonucleotide

<400> 51  
tcaggcgcgc cttgcccaca cagctgtgat c 31

<210> 52  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligonucleotide

<400> 52  
tcagggcgcgc ccttatctgg caggacctct 30

<210> 53  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligonucleotide

<400> 53

tcaggcgcg ctgcccgcg gcgc

25

<210> 54

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligonucleotide

<400> 54

ataaggcgcg ccctggcagg acctctcg

28